

Blast Result

EXHIBIT 2

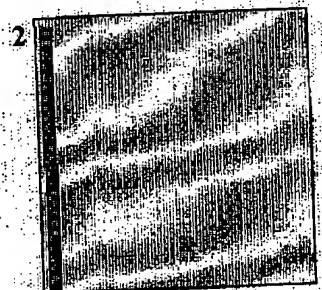
# NCBI Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]

Match: 1 Mismatch: 2 gap open: 5 gap extension: 2  
 x\_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 1 gi Homo sapiens endothelial differentiation, sphingolipid G- Length 2753 (1..2753)  
 13027635 protein-coupled receptor, 1 (EDG1), mRNA  
 Sequence 2 lcl|s\_q\_2 Length 25 (1..25)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 43.0 bits (22) Expect = 1.6  
 Identities = 14/25 (56%)  
 Strand = Plus / Minus

Query: 118 ctacacaaaaagcctggatcactca 142  
 |||||  
 Sbjct: 25 ctacacaaaaagcctggatcactca 1

CPU time: 0.06 user secs. 0.05 sys. secs 0.11 total secs.

Lambda K H  
 1.33 0.621 1.12

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Matrix: blast matrix: 1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 1

3/8/2002

## Blast Result

Number of Sequences: 0  
Number of extensions: 1  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
length of query: 2753  
length of database: 5,006,917,935  
effective HSP length: 25  
effective length of query: 2728  
effective length of database: 5,000,452,710  
effective search space: 13641234992880  
effective search space used: 13641234992880  
T: 0  
A: 30  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 21 (41.1 bits)